



Fig. 1

Nucleotide Sequence of the Clone #10

10 | 20 | 30 | 40 | 50 | 60 | 70 | 80 | 90 | 100
1 GCCACAGG CCCAGACTTT GACCTTCTT CACCACACT CCAGCTTCTT CCTGTAACT CACTGACCAC CGAAGACAGA TTCCACTCTT TACCTTCCAG 100
101 TCTACCAAG ATGCCCAATA CCATGGAG TATTGGCCAC AGTCCACTTT CTCTGTACGC CCAGTCTGTA ATGGAAGAGC TAACACTGC ACCCGTCCAA 200
201 GAGAGTCCAC CCTTGGCCAT GCCTCCTGGG AACTCACATG GTCTAGAGT GGGCTCATTT GCTGAGTTA AGGAGAACCC TCTTTCTAT GGGTAAATCC 300
301 GTTGGATCGG TCAGCCACCA GGACTGATG AGTGTCTGC TGGACTGGAA CTGGAAGATG AGTGTCTGC CTGTACGAT GGAACCTTCA GAGGCACTCG 400
401 GTATTTCACC TGTGCCCTGA AGAAGGCCCT GTTGTGAAA CTGAAGACT GCAGGCTGA CTCTAGTTT GCATCATTTG AGCCGTTTC CAATCAAGAT 500
501 TENGCCCTCT AACTCTTTAG CATTTGGAGG CTACTTTAGT GAGTGTGT;G AAGAAATPAC T:CCA:CCAA AATATGAAA AGAAGCTTG GAGATATGA 600
601 TTGGGAAG AGAAGGCA TCCAAGGCTC ATTCAATTC TTGTTACTTA G:ACTCAACC TTCTCTGCG TTATTTGCT TTTAGTCTG TTCTNGACA 700
701 CTGGTGTAC TTAGACCCC AAGAAAAAG AACGATGTT AGATATTTT NRTGEMACCC AAGAGTACT GAGGACAGAA ATGTGTATC CTCTGAGAT 800
801 ATATGATAT GTGTGTGCGA CAATAATAT GAACTGAGG AATACTTG AAAAGGTGA GCTGCTATCA GATTTTACCT CTGAAGAAA AGATCTCTGAG 900
901 GATTTCTTGA ATATCTGTT TACATATT TTAGGCTAG ACCTTTGCT AATAATAGA TCAGCAGGTC AAAGGTACA AGATGTATC TTCTATCAA 1000
1001 TTTTATGCA AAAAATGAG AAGTTGCGG TTCCACAAAT TCAGCAGTNG TTAGATGCT CTTTATCAA CAGTACCTG AATTTGCGG AGGCACCTC 1100
1101 ATGTCTGATT ATTCAGATGC CTCGATTTGG AAAAGACTTT AACTATTTA AAAATTTTT CTCTCTCTGG AATTAGATAT AACAGAGCAG TTTGTGAAA 1200
1201 CCCAGACAG TCCCGGATAT GTGAGGGCT TCCATATAT GAGTGTAAGA ATCTACGAC GATCCGACA CCAGCTGGAA AACAGAGCAG TTTGTGAAA 1300
1301 CCTGCAACAC TCAGTCCAC CTTCATCCGA AGAGCTGAA TCATATATAT AACCCAGTGT CACTTCCCA AGACTTACCC CGACTGGAG ATTGGAGACA 1400
1401 CGGCTGCATC CCTTGCAGA ATATGAGTT ATTTCTGTT CTCTGCAATG AACAGGCA CTATGTTGCT TTGTGAAAT ATGGGAGCA GATTTCTSC 1500
1501 TGGCTCTTCT TGGACAGCA TGGCCGATCC GGGATGGTGG TCAGATNGGC TCAACATTC CCCAGTCTC CHTGSCCCA GAGTAGGAG AGTACTTGA 1600
1601 AGATGCTTCC TGAAGACCC TGSATTCCT TGGATCCCA GGAGATCCC AAGCTGTGC AGAAGACTG CTTTGTGATG CCATATATGT GCCATGTACC 1700
1701 CAGAGTCAA CAATGATTT GTACAAATA CTGGGGTCA TCGGGAAGG CAAGAAGT GGAAGCAGA GTCCCTACG TTGCTCTTA TCGGAGCTG 1800
1801 GAGTCTGT TCACGTCCA TTGCGGCAA TGGATGCTTT TGTGGTATG ATCTTGAAGA AAGGAGGCC TGTGTTAAA AACAAATTC TTTGTGTC 1900
1901 CTGAAGTATT TAATAGAG CATTTGAC TCTAGAAAT AGTTTGTGT TGGTTTCTA AGAATCTAA ATGACTTAT TATACCTGA AGCTTAAAT 2000
2001 TAAGTGCATT GATCATAGA TATTTTGA AGCATACAT TTATATGTC GAATTTAAA GCCTTTTGA GTCCATGAG AATGTAAATA AATGTCTTT 2100
2101 CTTATGGA AAAA 2116



1 GGGTTTCT TTTACAC:TC T:CGGTACCG AACTCGGATC CACTAGTAAC GGGCCGCCAG TGTGCTGGAA ATTCGGCAGC AGGTGTGGG GAGCCGGGGC 100
101 CGGCCCGGA CGCGGGCTGG GGAGCCGGG CGAGGGCGGA CGGCCCGCG CCGGAGTTTC CCCCTTTCTA GGGTGAGGAT GGTCTACAC AGCCACCCCG 200
201 AGTTCCTTAG TTGAAGGTG CGCCTGCTG TGACAGAATG TGGTAATTGT AATCTTAAAC ATTTCATGT AAACATAIT TCTGTATCAT CTTTCCATTG 300
301 TCTTCATGGA AAATJGATAA AATTTTGTG CTTCCAACTC TCGTCTGGT TGAATGACTT CATCTTAATA CAACATGGAC ACCACGTTGC TGAACAACATG 400
401 CTTTGGGACT GCCACTGAAT TTAICTTTTG CGGTTTATG ACAAAGTTAT TAGTAGTTTC CCTTTTIGA ATTAGTATT TGAAGTTAAT ATCACAATGA 500
501 GTTCAGGCTT ATGGAGCCAA GAAAAAGTCA CTTCAACCTA CTGGGAAGAG CGGATTTTT ACTTGCTCT TCAAGAATGC AGCGTTACAG ACAAACAAC 600
601 ACAAAGCTC CTTAAAGTAC CGAAGGGAAG TATAGGACAG TATATTCAG ATCGTTCTGT GGGGCATTCA AGGATTCCTT CTGCAAAAGG CAAGAAAAAT 700
701 CAGATTGGAT TAAAAATTCT AGAGCAACCT CATGCAGTTC TCTTTGTGA TGAAGGAT GTTGATAGAGA TAAATGAAAA GTTCACAGAG TTACTTTTGG 800
801 CAATTACCAA TTGTAGGAG AGGTTACGCC TGTTTAAAAA CAGAAAGAGA CTAAAGTAAAG GCGTCCAAAT AGACGTGGGC TGTCTGTGA AAGTACAGCT 900
901 GAGATCTGG GAAGAAAAAT TTCTGGAGT TGTACGCTC AGAGGACCCC TGTAGCAGA GAGGACAGTC TCCGGAATAT TCTTTGGAGT TGAATTGCTG 1000
1001 GAAGNAGGTC GTGGTCAAGG TTCACTGAC GGGGTGTACC AAGGGAACA GCTTTTTCAG TGTGATGAAG ATTGTGGCGT GTTTGTGCA TTGGACAAGC 1100
1101 TAGAACTCAT AGAAGATGAT GACACTGCAT TGGAAAGTGA TTACGCAGGT CCTGGGGACA CAATGCAGGT CGAATTCCT CCTTTGGAAA TAACTCCAG 1200
1201 AGTTTCTTG AAGGTGGAG AAACAATAGA ATCTGGAACA GTTATATCT GTGATGTTT GCCAGGAAAA GAAAGCTTAG GATATTTTGT TGGTGGGAC 1300
1301 ATGGATAACC CTATTGGCAA CTGGGATGGA AGATTTGATG GAGTGCA:CT TTGTAGTTT GCGTGTGTTG AAAGTACAAT TCTATTGCAC ATCAATGATA 1400
1401 TCATCCCGA GAGTGTGACG CAGGAAAGGA GGCCTCCCA ACTTGCTTT ATGTCAAGAG GTGTTGGGA CAAAGGTTC TCCAGTTCATA ATAAACCAA 1500
1501 GGCTACAGGA TCTACCTCAG ACCCTGGAAA TAGAAMCAGA TGTGAATTAT TTTATACCTT AAATGGGTCT TCTGTGACT CACAACCACA ATCCAAATCA 1600
1601 AAAAATACAT GGTACATTGA TGAAGTTGCA GAAGACCTG CAAAATCTCT TACAGAGATA TCTACAGACT TTACCGTTC TTCACCAOCA CTCGAGCTC 1700
1701 CTCTGTGAA CTCACTGACC ACCGAGAACA GATTCACCTC TTACCATTC AGTCCACCA AGATGCCAA TACCAATGGA AGTATTGGCC ACAGTCCACT 1800
1801 TTCTGTGCA GCCCAGTCTG TAATGGAAGA GCTAAACACT GCACCCGTCC AAGAGAGTCC ACCCTTGGCC ATGCTCTCTG GGAACCTACA TGGTCTAGAA 1900
1901 GTGGGCTCAT TGGCTGAAGT TAAGGAGAAC CCTCCTTTCT ATGGGGTAAT CCGTTGGATC GGTACGCCAC CAGGACTGAA TGAAGTGCTC CCGGACTGG 2000
2001 AACTGGAAGA TGAGTGTGCA GGCTGTACGG ATGGAACCTT CAGAGGCACT CGGTATTTCA CCTGTGCCCT GAAGAAGCG CTGTTTGA AACTGAAGAG 2100
2101 CTGAGGCT GACTCTAGGT TTGCATCAIT GCAGCCGTTT TCCAATCAGA TTGAGCGCTG TAACTCTTTA GCATTGGAG GCTACTTAAG TGAAGTAGTA 2200
2201 GAAGAAAAATA CTCACCAAAA AATGGA AAAA GAAGGCTTGG AGATAATGAT TGGGAAGAAG AAAGGCATCC AGGGCTATTA CAATCTTGT TACTTAGACT 2300
2301 CAACCTTATT CTGCTTATT GCTTTTAGT CTGTTCTGGA CACTGTGTTA CTAGACCCA AAGAAAAAGAA CGATGTAGAA TATTATAGT AAACCCAAGA 2400

21
12
13
2



2401 GCTACTGAGG ACAGAAATTG TTAATCCCTCT GAGAATATATGGATATGTGT GTGCCACAAA AATTATGAAA CTGAGGAAAA TACTTTGAAAA GGTGGAGGCT 2500
2501 GCATCAGGAT TTACCTCTGA AGAAAAAGAT CCTGAGGAAT TCTTGAATAT TCTGTTTCAT CATAITTTAA GGGTAGAAACC TTGCTAAAA ATAAGATCAG 2600
2601 CAGGTCAAAA GGTACAAGAT TGTACTTCT ATCAAAATTT TATGGAAAAA AATGAGAAAAG TTGGCGTTCC CACAATTCAG CAGTTGTTAG AATGGTCTTT 2700
2701 TATCAACAGT AACCTGAAAT TTGCAGAGGC ACCATCATGT CTGATTATTC AGATGCCCTCG AATTGGAAAA GACTTTAAAC TATTTAAAAA AATTTTCTCT 2800
2801 TCTCTGGAAT TAAATATAAC AGATTTACTT GAAGACACTC CCAGACAGTG CCGGATATGT GGAGGGCTTG CAATGTATGA GTGTAGAGAA TGCTACGACG 2900
2901 ATCCGGACAT CTCAGCTGGA AAAATCAAGC AGTTTGTAA AACCTGCAAC ACTCAAGTCC ACCTTCATCC GAAGAGGCTG AATCATAAAT ATAAACCCAGT 3000
3001 GTCACCTTCCC AAAGACTTAC CCGACTGGGA CTGGAGACAC GGCTGCATCC CTTGCCAGAA TATGGAGTTA TTTGCTGTTT TCTGCATAGA AACAAGCCAC 3100
3101 TATGTTGCTT TTGTGAAGTA TGGGAAGGAC GATTCTGCCT GGCTCTTCTT TGACAGCATG GCCGATCGGG ATGGTGGTCA GAATGGCTTC AACATTCCTC 3200
3201 AAGTCACCC ATGCCCAGAA GTAGGAGAGT ACTTGAAGAT GTCTCTGGAA GACCTGCATT CCTTGGACTC CAGGAGAAATC CAAGGCTGTG CACGAAGACT 3300
3301 GCTTTGTGAT GCATATATGT GCATGTACCA GAGTCCAACA ATGAGTTTGT ACAATAACT GGGGTCACTG GGAAGGCAA AGAAACTGAA GGCAGAGTCC 3400
3401 TAACGTTGCA TCTTATTGGA GCTGGCAGTT CTGTTACGT CCATTGCCCG CAATGGATGT CTTTGTGGTG ATGATCCCTC AGAAAAGGAT GCCTCTGTTT 3500
3501 AAAAACAAT TGCCTTTGTG TCCCTGAAAT ATTTAATAAG AAGCATTTTG CACTTAGAA AGIATGTTTG TGTGCTTTT TTAAGAAGTC TAAATGAAGT 3600
3601 TATTAAATACC TGAAGCTTTA AGTTAAGTGC ATTGATCATA TGATAATTTT GGAAGCATAC AATTTAAT GTGGAAGTTT AAAGCCTCTT TTAGTCCATT 3700
3701 GAGAATGTAA ATAAA

3715

Fig. 2 (cont.)



8	NSS	GLMSQEKVTS	PYWEERIFYL	LLQECSTDK	QFQKLLKVPK	GSIGQYIQDR	SVGHSRIPSA	KGKKNQIGLK	ILEQPHAVLF	VDEDVVEINE	100
101	KFTELLALIT	NCEERFSLFK	NRNRLSKGLQ	IDVGCVPKVQ	LRSGEKFTPG	VRFRGPLLA	EXTVSGIFFG	VELLECGRQ	GFTDGVYQ GK	QLFQCEDCG	200
201	FVALDKLEL	IEDDDTALES	DYAGFGDTMQ	VELPPLEINS	RVSLKGGETI	ESGTVIFCDV	LPKESLGYF	VGVDMDNPIG	NWDGRFDGVL	CSPACVESTI	300
301	LLHINDIPE	SVTOERRPPK	LAFMSRGVGD	KGSSSHNPKK	ATGSTSDPGN	RRSELYFTLN	GSSVDSQPOS	KSKNTWYIDE	VAEDPAKSLT	EISTDFDRSS	400
401	PPIQPPPPUNS	LTTEHREHSL	PFSITKMENT	NGSIGHSPLS	LSAQSVMEEL	NTAPVQESPP	LAMPFGNSHG	LEVGSLEAVK	ENPPFYGVIR	WIGQPPGLNE	500
501	VLAGLELEDE	CAGCTDGTFR	GTRYFTCALK	KALFVKLKSC	RPDSRFASLQ	PVSNQIERCN	SLAFGGYLSE	VVEENTPPRM	EREGLEIMIG	KKKGIQGHYN	600
601	SCYLDSTLFC	LEAFSSVLDT	VLLRPKEKND	VEYYSETQEL	LRTEIVNPLR	IYGVVCATKI	MKLRLKILEKV	EAASGTSEE	KDPEEFLNIL	FHHILRVEPL	700
701	LKIRSAGOKV	QDCYFYQIEM	ERKEKVGVP	IQOLLEWSFI	NSNLKEAEAP	SCLTIQMPRF	GRDEKLFKKI	FPSLELNITD	LLEDTPROCR	ICGGLAWYEC	800
801	RECYDDPDIS	AGKIKQFCKT	CNTQVHLHPK	RINHKNYPVS	LPKDLDPDWN	RHGCIPCONM	ELFAVLICLET	SHYVAFVKYG	KDSSAWLFFD	SKADRDGGSQ	900
901	GNIPQVTPC	PEVGEYLKNS	LEDLHSLDSR	RIQGCARRLL	CDAYMCNYQS	PTWSLYK					957

Fig. 3